

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/526,234 A
Source: IFWP
Date Processed by STIC: 08/04/2006

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 08/04/2006

PATENT APPLICATION: US/10/526,234A

TIME: 13:04:59

Input Set : A:\3190-072 Sequence Listing.txt

Output Set: N:\CRF4\08042006\J526234A.raw

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3 <110> APPLICANT: DOI, Hirofumi
4      KUDO, Gen
6 <120> TITLE OF INVENTION: Method of Degradation, Method for Inhibiting
Degradation,
7      and Agent for Inhibiting Degradation, for Transcription
8      Factors of Glucose Metabolism-Related Genes
10 <130> FILE REFERENCE: 3190-072
12 <140> CURRENT APPLICATION NUMBER: 10/526,234A
13 <141> CURRENT FILING DATE: 2005-02-28
15 <150> PRIOR APPLICATION NUMBER: PCT/JP2003/11046
16 <151> PRIOR FILING DATE: 2003-08-29
19 <150> PRIOR APPLICATION NUMBER: JP P2002-254973
20 <151> PRIOR FILING DATE: 2002-08-30
22 <150> PRIOR APPLICATION NUMBER: JP P2003-96370
23 <151> PRIOR FILING DATE: 2003-03-31
25 <150> PRIOR APPLICATION NUMBER: JP P2003-96371
26 <151> PRIOR FILING DATE: 2003-03-31
28 <150> PRIOR APPLICATION NUMBER: JP P2003-96372
29 <151> PRIOR FILING DATE: 2003-03-31
31 <160> NUMBER OF SEQ ID NOS: 5
33 <170> SOFTWARE: PatentIn version 3.1
35 <210> SEQ ID NO: 1
36 <211> LENGTH: 465
37 <212> TYPE: PRT
38 <213> ORGANISM: Homo sapiens
40 <400> SEQUENCE: 1
42 Met Asp Met Ala Asp Tyr Ser Ala Ala Leu Asp Pro Ala Tyr Thr Thr
43 1      5      10      15
46 Leu Glu Phe Glu Asn Val Gln Val Leu Thr Met Gly Asn Asp Thr Ser
47      20      25      30
50 Pro Ser Glu Gly Thr Asn Leu Asn Ala Pro Asn Ser Leu Gly Val Ser
51      35      40      45
54 Ala Leu Cys Ala Ile Cys Gly Asp Arg Ala Thr Gly Lys His Tyr Gly
55      50      55      60
62 Ala Ser Ser Cys Asp Gly Cys Lys Gly Phe Phe Arg Arg Ser Val Arg
63 65      70      75      80
66 Lys Asn His Met Tyr Ser Cys Arg Phe Ser Arg Gln Cys Val Val Asp
67      85      90      95
70 Lys Asp Lys Arg Asn Gln Cys Arg Tyr Cys Arg Leu Lys Lys Cys Phe
71      100     105     110
74 Arg Ala Gly Met Lys Lys Glu Ala Val Gln Asn Glu Arg Asp Arg Ile
75      115     120     125
78 Ser Thr Arg Arg Ser Ser Tyr Glu Asp Ser Ser Leu Pro Ser Ile Asn
79      130     135     140

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```

82 Ala Leu Leu Gln Ala Glu Val Leu Ser Arg Gln Ile Thr Ser Pro Val
83 145                      150                      155                      160
86 Ser Gly Ile Asn Gly Asp Ile Arg Ala Lys Lys Ile Ala Ser Ile Ala
87                      165                      170                      175
90 Asp Val Cys Glu Ser Met Lys Glu Gln Leu Leu Val Leu Val Glu Trp
91                      180                      185                      190
94 Ala Lys Tyr Ile Pro Ala Phe Cys Glu Leu Pro Leu Asp Asp Gln Val
95                      195                      200                      205
98 Ala Leu Leu Arg Ala His Ala Gly Glu His Leu Leu Leu Gly Ala Thr
99      210                      215                      220
102 Lys Arg Ser Met Val Phe Lys Asp Val Leu Leu Leu Gly Asn Asp Tyr
103 225                      230                      235                      240
106 Ile Val Pro Arg His Cys Pro Glu Leu Ala Glu Met Ser Arg Val Ser
107                      245                      250                      255
110 Ile Arg Ile Leu Asp Glu Leu Val Leu Pro Phe Gln Glu Leu Gln Ile
111                      260                      265                      270
114 Asp Asp Asn Glu Tyr Ala Tyr Leu Lys Ala Ile Ile Phe Phe Asp Pro
115                      275                      280                      285
119 Asp Ala Lys Gly Leu Ser Asp Pro Gly Lys Ile Lys Arg Leu Arg Ser
120                      290                      295                      300
123 Gln Val Gln Val Ser Leu Glu Asp Tyr Ile Asn Asp Arg Gln Tyr Asp
124 305                      310                      315                      320
127 Ser Arg Gly Arg Phe Gly Glu Leu Leu Leu Leu Leu Pro Thr Leu Gln
128                      325                      330                      335
131 Ser Ile Thr Trp Gln Met Ile Glu Gln Ile Gln Phe Ile Lys Leu Phe
132                      340                      345                      350
135 Gly Met Ala Lys Ile Asp Asn Leu Leu Gln Glu Met Leu Leu Gly Gly
136                      355                      360                      365
139 Ser Pro Ser Asp Ala Pro His Ala His His Pro Leu His Pro His Leu
140                      370                      375                      380
143 Met Gln Glu His Met Gly Thr Asn Val Ile Val Ala Asn Thr Met Pro
144 385                      390                      395                      400
147 Thr His Leu Ser Asn Gly Gln Met Cys Glu Trp Pro Arg Pro Arg Gly
148                      405                      410                      415
151 Gln Ala Ala Thr Pro Glu Thr Pro Gln Pro Ser Pro Pro Gly Gly Ser
152                      420                      425                      430
155 Gly Ser Glu Pro Tyr Lys Leu Leu Pro Gly Ala Val Ala Thr Ile Val
156                      435                      440                      445
159 Lys Pro Leu Ser Ala Ile Pro Gln Pro Thr Ile Thr Lys Gln Glu Val
160                      450                      455                      460
163 Ile
164 465
167 <210> SEQ ID NO: 2
168 <211> LENGTH: 631
169 <212> TYPE: PRT
170 <213> ORGANISM: Homo sapiens
173 <220> FEATURE:
174 <221> NAME/KEY: MISC_FEATURE
176 <222> LOCATION: (322)..(322)

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177 <223> OTHER INFORMATION: UNSURE

178 Xaa may be Tyr since it has been shown in many reports

179 that the codon of Xaa is tat.

182 <400> SEQUENCE: 2

184 Met Val Ser Lys Leu Ser Gln Leu Gln Thr Glu Leu Leu Ala Ala Leu

185 1 5 10 15

188 Leu Glu Ser Gly Leu Ser Lys Glu Ala Leu Ile Gln Ala Leu Gly Glu

189 20 25 30

192 Pro Gly Pro Tyr Leu Leu Ala Gly Glu Gly Pro Leu Asp Lys Gly Glu

193 35 40 45

196 Ser Cys Gly Gly Gly Arg Gly Glu Leu Ala Glu Leu Pro Asn Gly Leu

197 50 55 60

200 Gly Glu Thr Arg Gly Ser Glu Asp Glu Thr Asp Asp Asp Gly Glu Asp

201 65 70 75 80

204 Phe Thr Pro Pro Ile Leu Lys Glu Leu Glu Asn Leu Ser Pro Glu Glu

205 85 90 95

208 Ala Ala His Gln Lys Ala Val Val Glu Thr Leu Leu Gln Glu Asp Pro

209 100 105 110

212 Trp Arg Val Ala Lys Met Val Lys Ser Tyr Leu Gln Gln His Asn Ile

213 115 120 125

216 Pro Gln Arg Glu Val Val Asp Thr Thr Gly Leu Asn Gln Ser His Leu

217 130 135 140

220 Ser Gln His Leu Asn Lys Gly Thr Pro Met Lys Thr Gln Lys Arg Ala

221 145 150 155 160

224 Ala Leu Tyr Thr Trp Tyr Val Arg Lys Gln Arg Glu Val Ala Gln Gln

225 165 170 175

228 Phe Thr His Ala Gly Gln Gly Gly Leu Ile Glu Glu Pro Thr Gly Asp

229 180 185 190

233 Glu Leu Pro Thr Lys Lys Gly Arg Arg Asn Arg Phe Lys Trp Gly Pro

234 195 200 205

237 Ala Ser Gln Gln Ile Leu Phe Gln Ala Tyr Glu Arg Gln Lys Asn Pro

238 210 215 220

241 Ser Lys Glu Glu Arg Glu Thr Leu Val Glu Glu Cys Asn Arg Ala Glu

242 225 230 235 240

245 Cys Ile Gln Arg Gly Val Ser Pro Ser Gln Ala Gln Gly Leu Gly Ser

246 245 250 255

249 Asn Leu Val Thr Glu Val Arg Val Tyr Asn Trp Phe Ala Asn Arg Arg

250 260 265 270

253 Lys Glu Glu Ala Phe Arg His Lys Leu Ala Met Asp Thr Tyr Ser Gly

254 275 280 285

257 Pro Pro Pro Gly Pro Gly Pro Gly Pro Ala Leu Pro Ala His Ser Ser

258 290 295 300

262 Pro Gly Leu Pro Pro Pro Ala Leu Ser Pro Ser Lys Val His Gly Val

263 305 310 315 320

W--> 266 Arg Xaa Gly Gln Pro Ala Thr Ser Glu Thr Ala Glu Val Pro Ser Ser

267 325 330 335

270 Ser Gly Gly Pro Leu Val Thr Val Ser Thr Pro Leu His Gln Val Ser

271 340 345 350

274 Pro Thr Gly Leu Glu Pro Ser His Ser Leu Leu Ser Thr Glu Ala Lys

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275          355          360          365
278 Leu Val Ser Ala Ala Gly Gly Pro Leu Pro Pro Val Ser Thr Leu Thr
279          370          375          380
282 Ala Leu His Ser Leu Glu Gln Thr Ser Pro Gly Leu Asn Gln Gln Pro
283 385          390          395          400
286 Gln Asn Leu Ile Met Ala Ser Leu Pro Gly Val Met Thr Ile Gly Pro
287          405          410          415
294 Gly Glu Pro Ala Ser Leu Gly Pro Thr Phe Thr Asn Thr Gly Ala Ser
295          420          425          430
298 Thr Leu Val Ile Gly Leu Ala Ser Thr Gln Ala Gln Ser Val Pro Val
299          435          440          445
302 Ile Asn Ser Met Gly Ser Ser Leu Thr Thr Leu Gln Pro Val Gln Phe
303          450          455          460
306 Ser Gln Pro Leu His Pro Ser Tyr Gln Gln Pro Leu Met Pro Pro Val
307 465          470          475          480
310 Gln Ser His Val Thr Gln Ser Pro Phe Met Ala Thr Met Ala Gln Leu
311          485          490          495
314 Gln Ser Pro His Ala Leu Tyr Ser His Lys Pro Glu Val Ala Gln Tyr
315          500          505          510
318 Thr His Thr Gly Leu Leu Pro Gln Thr Met Leu Ile Thr Asp Thr Thr
319          515          520          525
322 Asn Leu Ser Ala Leu Ala Ser Leu Thr Pro Thr Lys Gln Val Phe Thr
323          530          535          540
326 Ser Asp Thr Glu Ala Ser Ser Glu Ser Gly Leu His Thr Pro Ala Ser
327 545          550          555          560
330 Gln Ala Thr Thr Leu His Val Pro Ser Gln Asp Pro Ala Gly Ile Gln
331          565          570          575
334 His Leu Gln Pro Ala His Arg Leu Ser Ala Ser Pro Thr Val Ser Ser
335          580          585          590
338 Ser Ser Leu Val Leu Tyr Gln Ser Ser Asp Ser Ser Asn Gly Gln Ser
339          595          600          605
342 His Leu Leu Pro Ser Asn His Ser Val Ile Glu Thr Phe Ile Ser Thr
343          610          615          620
346 Gln Met Ala Ser Ser Ser Gln
347 625          630
353 <210> SEQ ID NO: 3
354 <211> LENGTH: 283
355 <212> TYPE: PRT
356 <213> ORGANISM: Homo sapiens
358 <400> SEQUENCE: 3
360 Met Asn Gly Glu Glu Gln Tyr Tyr Ala Ala Thr Gln Leu Tyr Lys Asp
361 1          5          10          15
364 Pro Cys Ala Phe Gln Arg Gly Pro Ala Pro Glu Phe Ser Ala Ser Pro
365          20          25          30
368 Pro Ala Cys Leu Tyr Met Gly Arg Gln Pro Pro Pro Pro Pro Pro His
369          35          40          45
372 Pro Phe Pro Gly Ala Leu Gly Ala Leu Glu Gln Gly Ser Pro Pro Asp
373          50          55          60
376 Ile Ser Pro Tyr Glu Val Pro Pro Leu Ala Asp Asp Pro Ala Val Ala

```

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```

377 65              70              75              80
380 His Leu His His His Leu Pro Ala Gln Leu Ala Leu Pro His Pro Pro
381              85              90              95
384 Ala Gly Pro Phe Pro Glu Gly Ala Glu Pro Gly Val Leu Glu Glu Pro
385              100              105              110
388 Asn Arg Val Gln Leu Pro Phe Pro Trp Met Lys Ser Thr Lys Ala His
389              115              120              125
392 Ala Trp Lys Gly Gln Trp Ala Gly Gly Ala Tyr Ala Ala Glu Pro Glu
393              130              135              140
396 Glu Asn Lys Arg Thr Arg Thr Ala Tyr Thr Arg Ala Gln Leu Leu Glu
397 145              150              155              160
400 Leu Glu Lys Glu Phe Leu Phe Asn Lys Tyr Ile Ser Arg Pro Arg Arg
401              165              170              175
404 Val Glu Leu Ala Val Met Leu Asn Leu Thr Glu Arg His Ile Lys Ile
405              180              185              190
411 Trp Phe Gln Asn Arg Arg Met Lys Trp Lys Lys Glu Glu Asp Lys Lys
412              195              200              205
415 Arg Gly Gly Gly Thr Ala Val Gly Gly Gly Gly Val Ala Glu Pro Glu
416              210              215              220
419 Gln Asp Cys Ala Val Thr Ser Gly Glu Glu Leu Leu Ala Leu Pro Pro
420 225              230              235              240
423 Pro Pro Pro Pro Gly Gly Ala Val Pro Pro Ala Ala Pro Val Ala Ala
424              245              250              255
427 Arg Glu Gly Arg Leu Pro Pro Gly Leu Ser Ala Ser Pro Gln Pro Ser
428              260              265              270
431 Ser Val Ala Pro Arg Arg Pro Gln Glu Pro Arg
432              275              280
435 <210> SEQ ID NO: 4
436 <211> LENGTH: 6
437 <212> TYPE: PRT
438 <213> ORGANISM: Homo sapiens
440 <220> FEATURE:
441 <221> NAME/KEY: MISC_FEATURE
442 <223> OTHER INFORMATION: Partial peptide of human m-calpain or rabbit m-
calpain, showing high
443     score in the local alignment between human m-calpain or rabbit
444     m-calpain and human HNF-4alpha
447 <400> SEQUENCE: 4
449 Phe Lys Leu Pro Pro Gly
450 1              5
452 <210> SEQ ID NO: 5
453 <211> LENGTH: 6
454 <212> TYPE: PRT
455 <213> ORGANISM: Homo sapiens
457 <220> FEATURE:
458 <221> NAME/KEY: misc_feature
459 <223> OTHER INFORMATION: Partial peptide of human HNF-4alpha, showing high
score in the
460     local alignment between human m-calpain or rabbit m-calpain and
461     human HNF-4alpha
463 <400> SEQUENCE: 5

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/526,234A

DATE: 08/04/2006
TIME: 13:05:00

Input Set : A:\3190-072 Sequence Listing.txt
Output Set: N:\CRF4\08042006\J526234A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; Xaa Pos. 322

VERIFICATION SUMMARY

DATE: 08/04/2006

PATENT APPLICATION: US/10/526,234A

TIME: 13:05:00

Input Set : A:\3190-072 Sequence Listing.txt

Output Set: N:\CRF4\08042006\J526234A.raw

L:266 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:320